

459/498

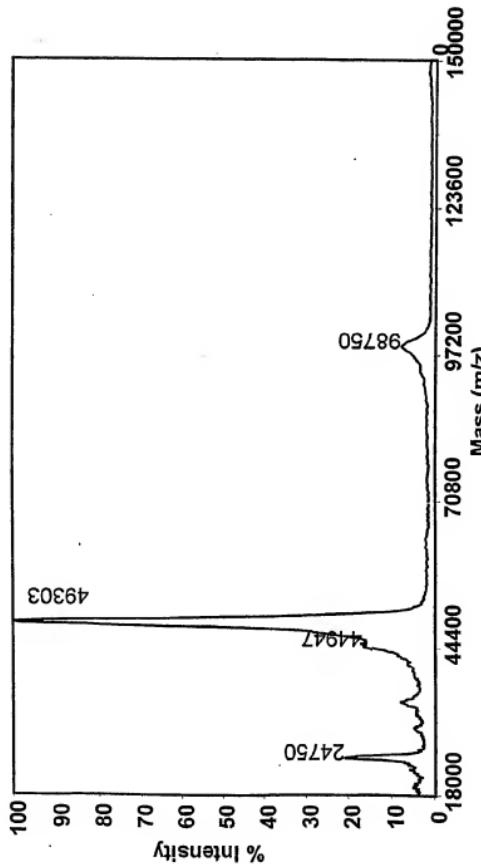


FIG. 158

460/498

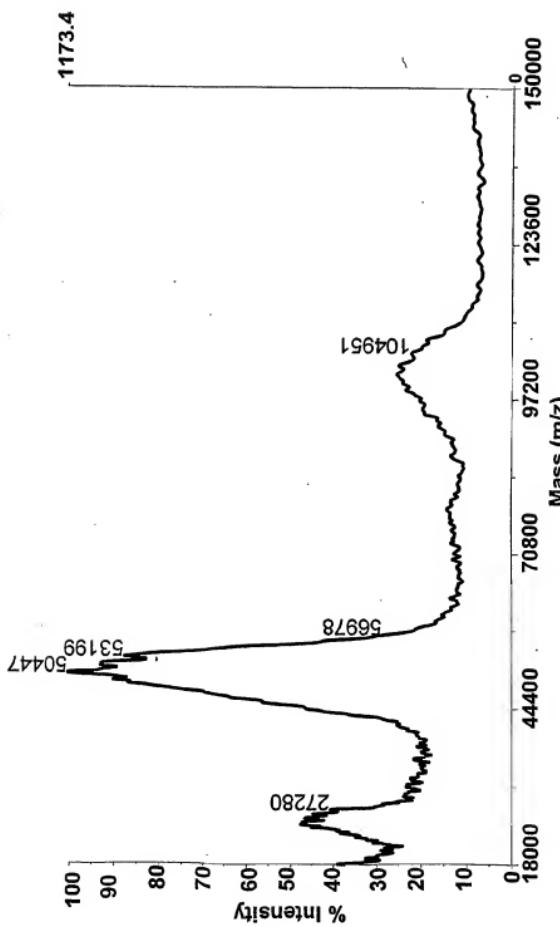


FIG. 159

461/498

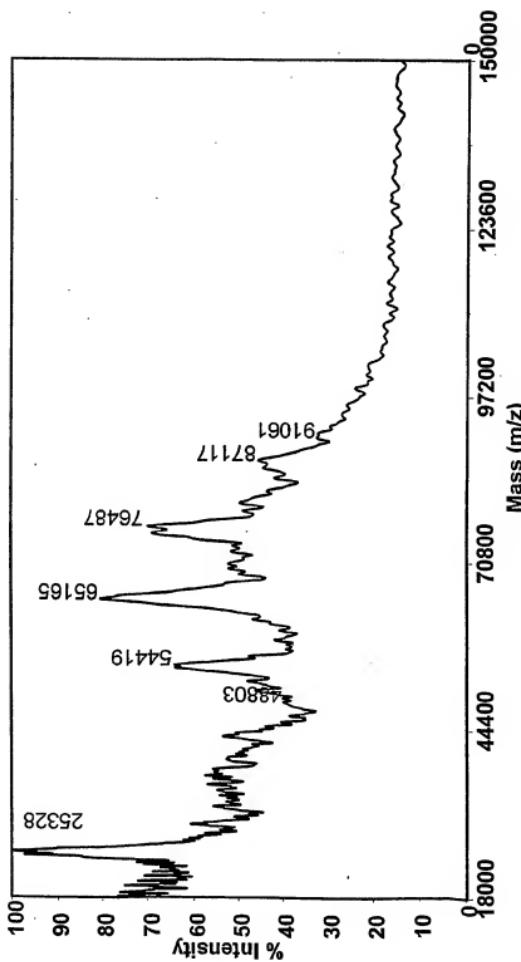


FIG. 160

462/498

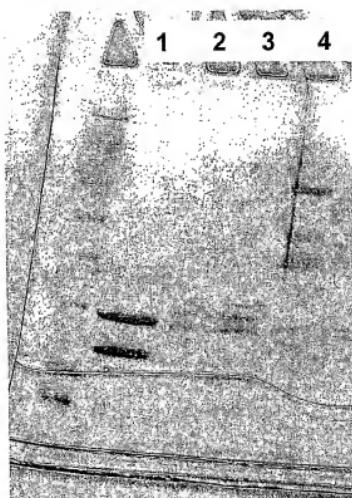


FIG. 161

463/498

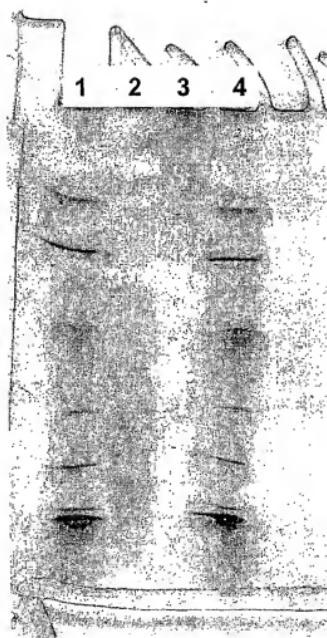


FIG. 162

464/498

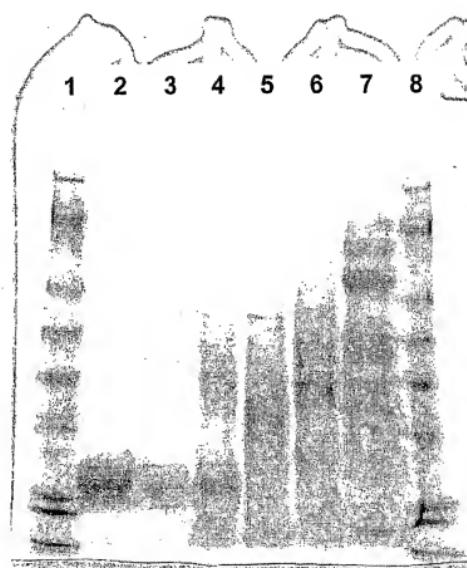


FIG. 163

465/498

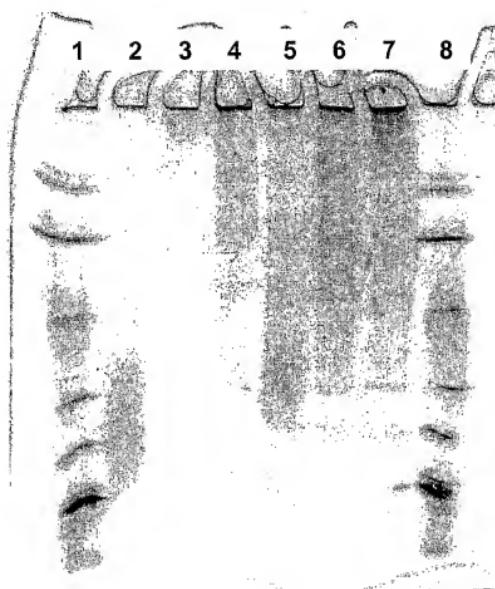


FIG. 164

466/498

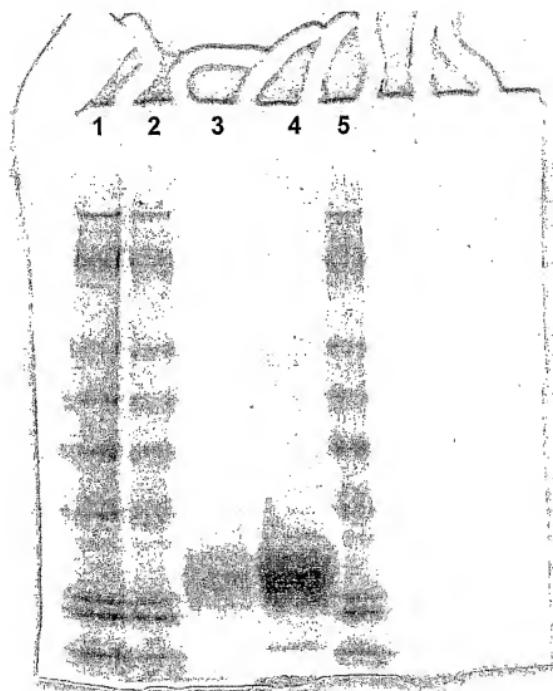


FIG. 165

467/498

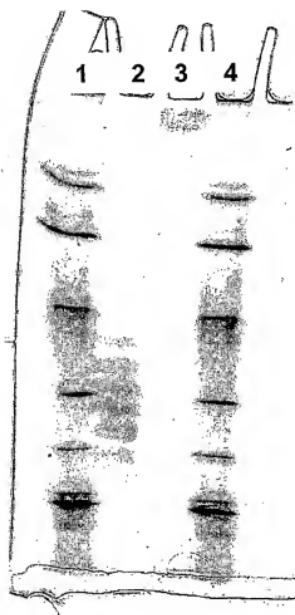


FIG. 166

468/498

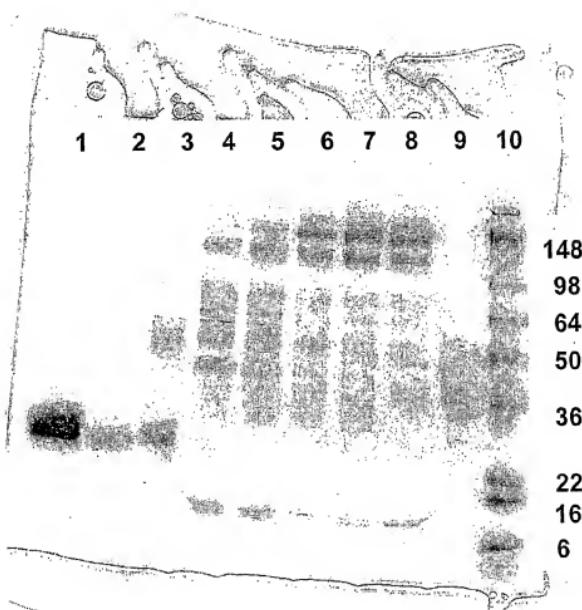


FIG. 167

469/498

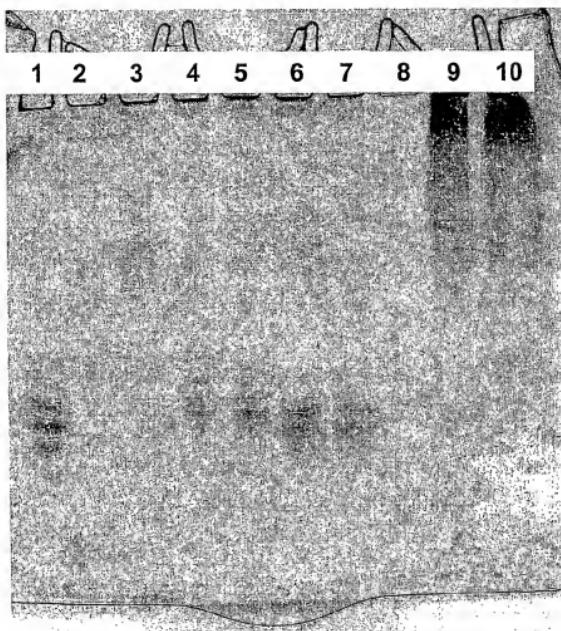


FIG. 168

470/498

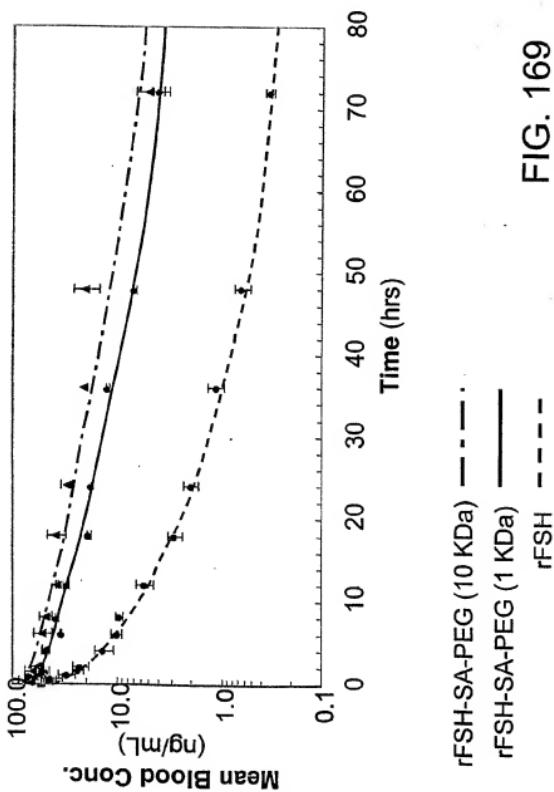


FIG. 169

471/498

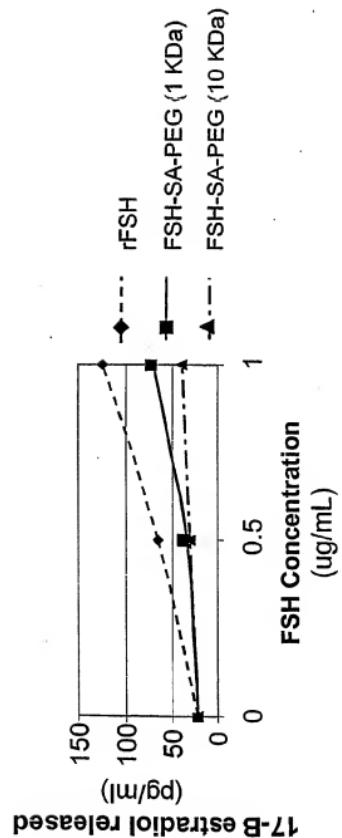


FIG. 170

472/498

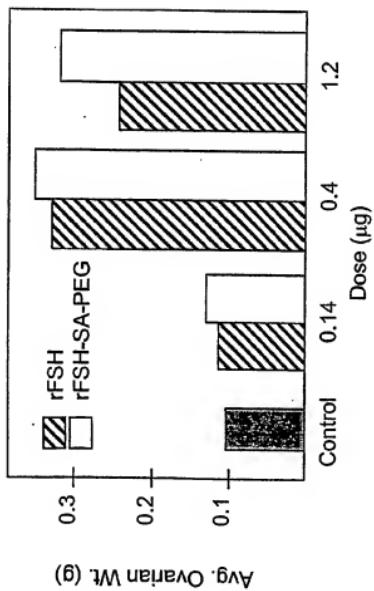


FIG. 171

473/498

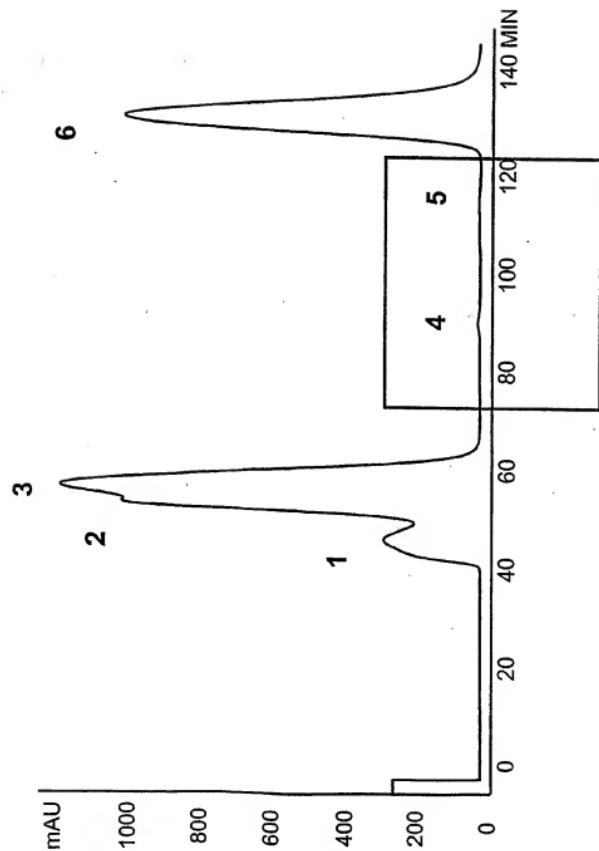


FIG. 172A

474/498

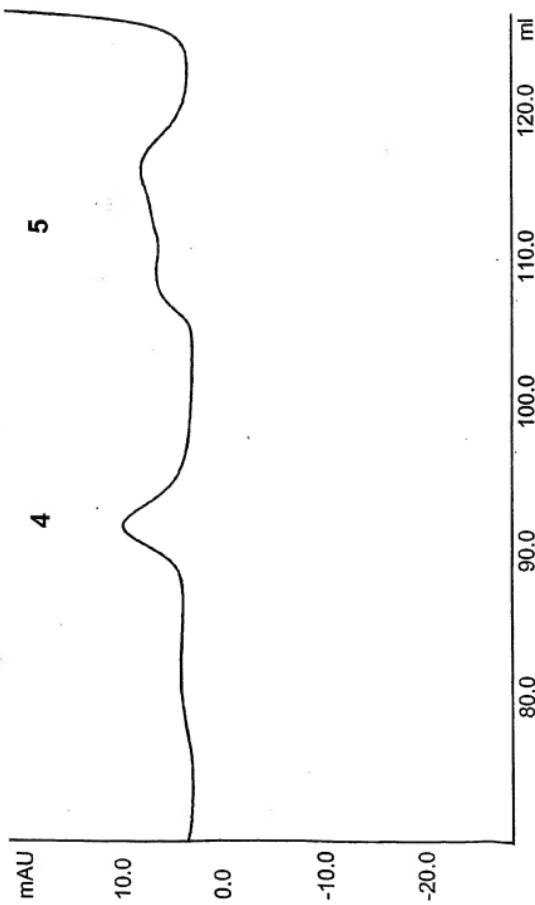


FIG. 172B

475/498

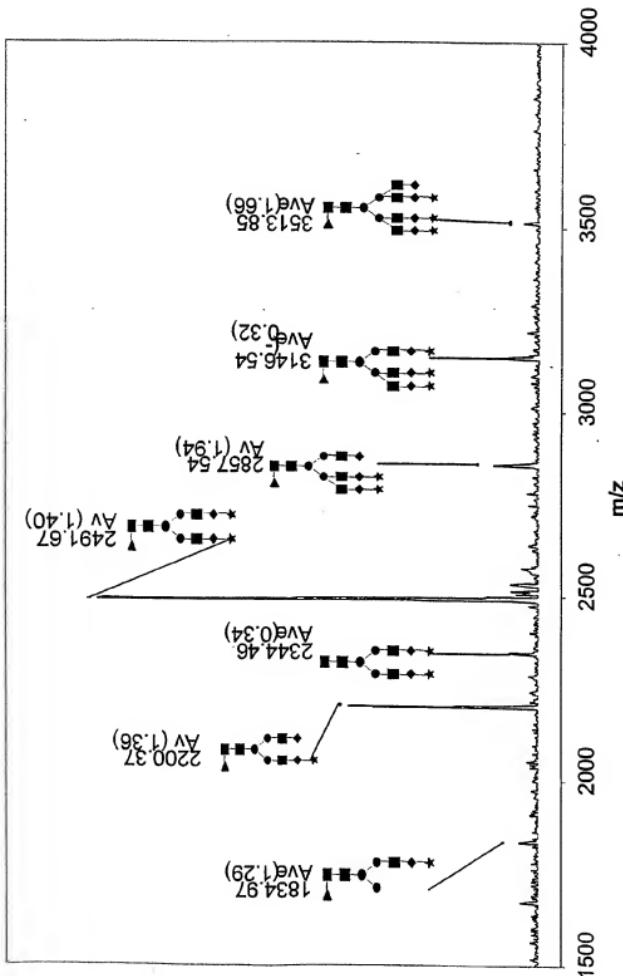


FIG. 173A

476/498

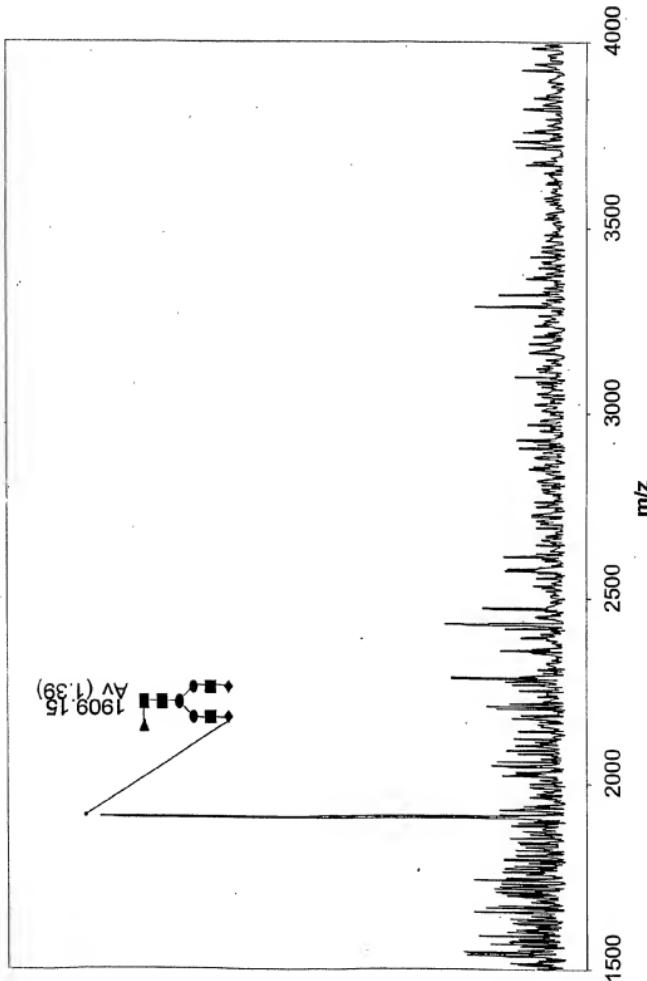


FIG. 173B

477/498

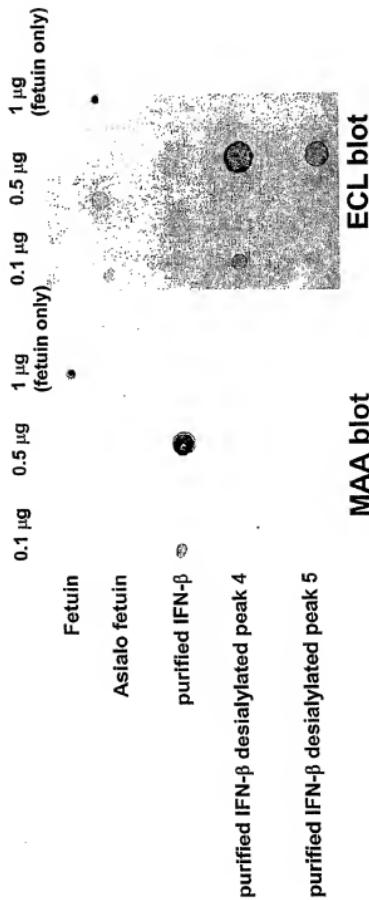


FIG. 174

478/498

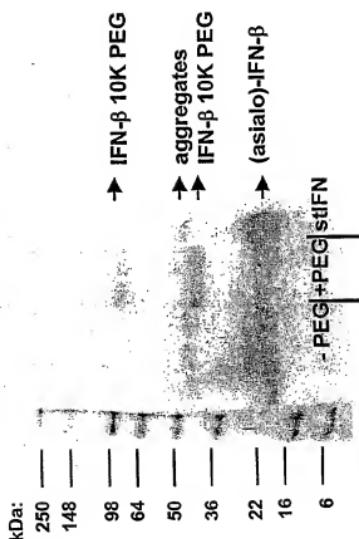
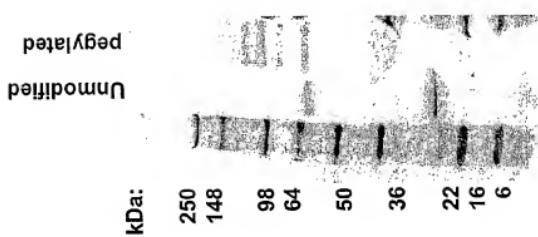


FIG. 175

479/498

FIG. 176



480/498

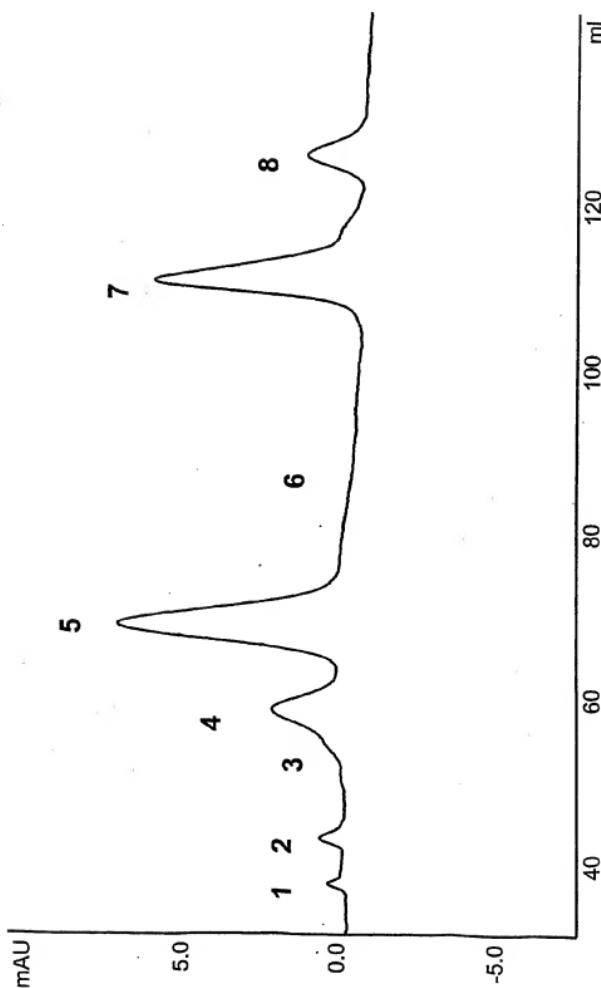


FIG. 177

481/498

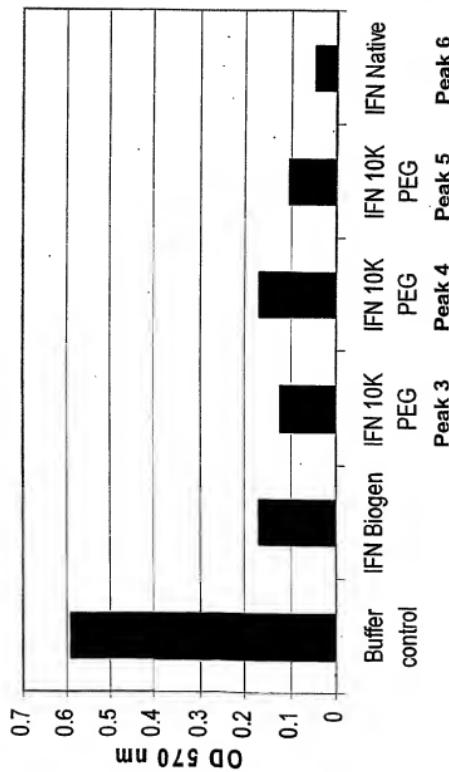


FIG. 178

482/498

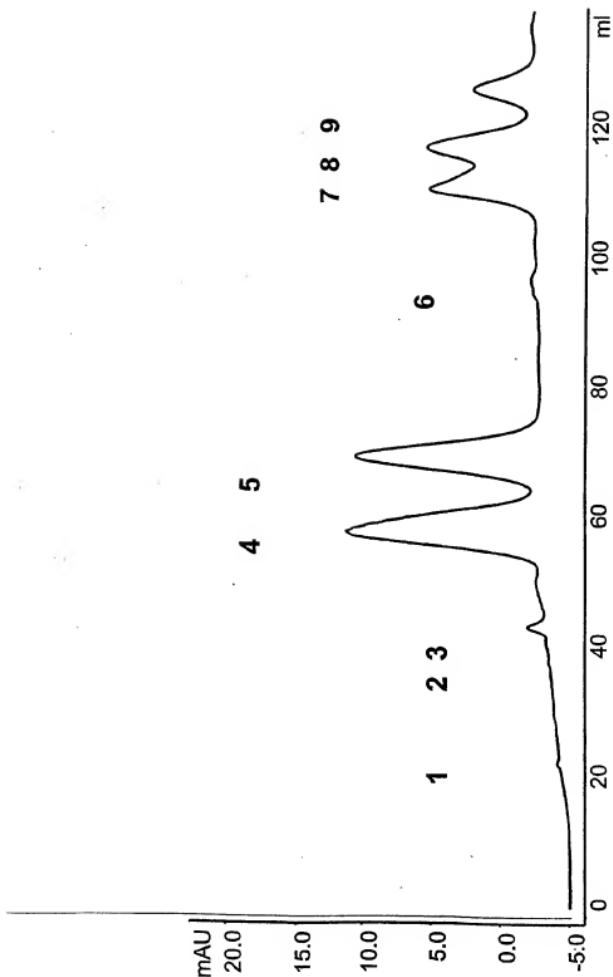


FIG. 179

483/498

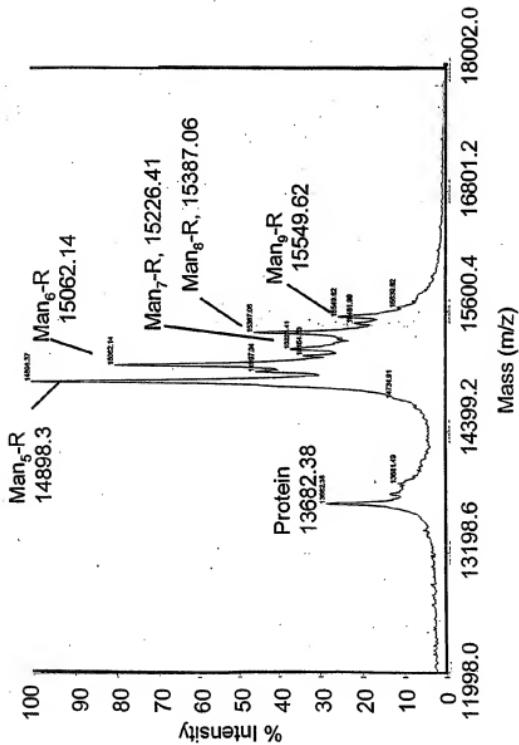


FIG. 180A

484/498

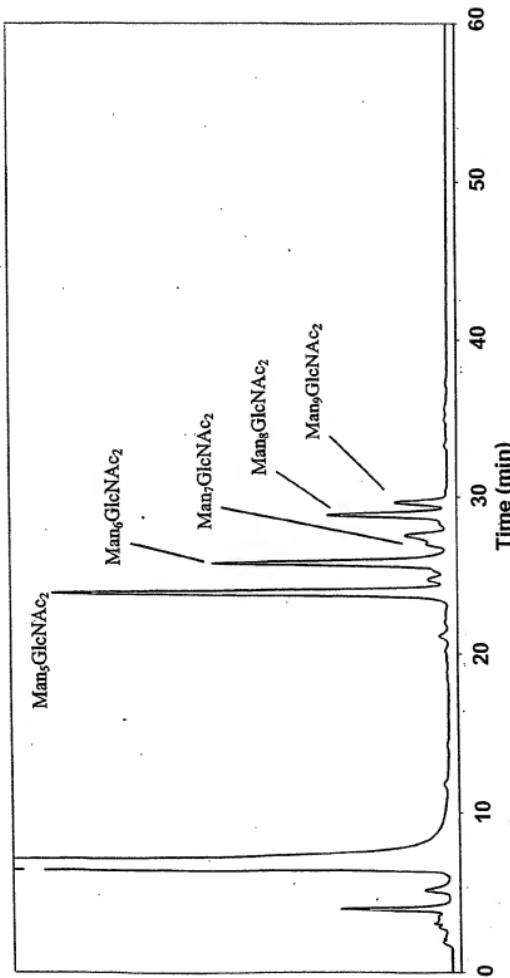


FIG. 180B

485/498

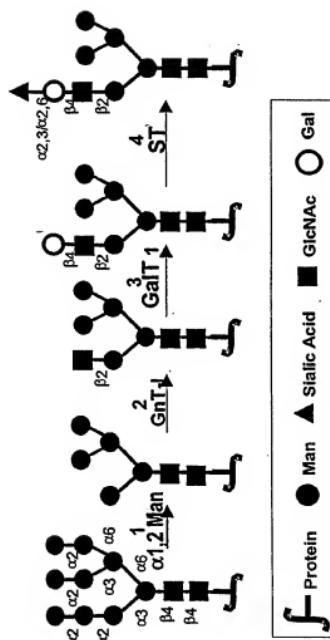


FIG. 181

486/498

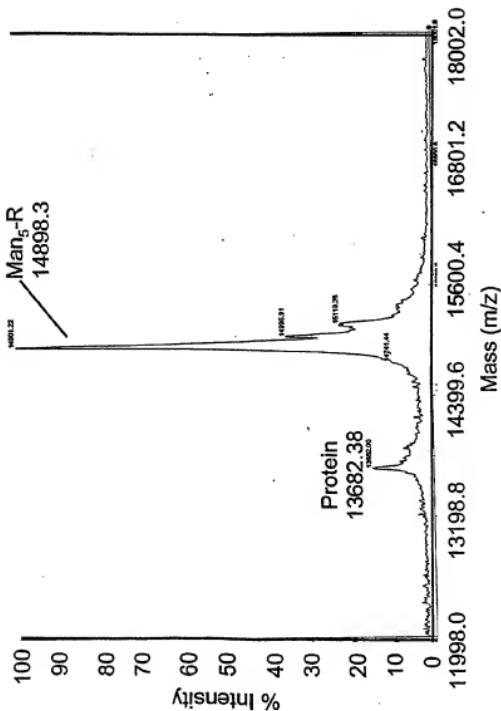


FIG. 182A

487/498

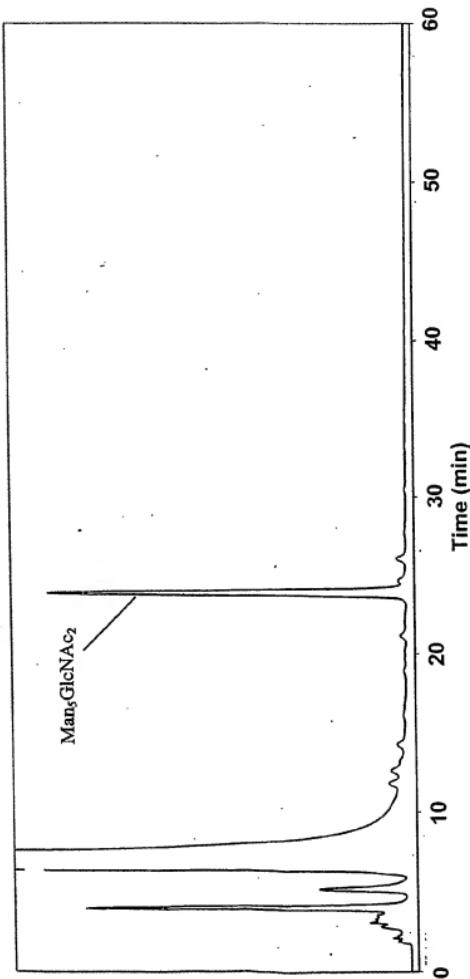


FIG. 182B

488/498

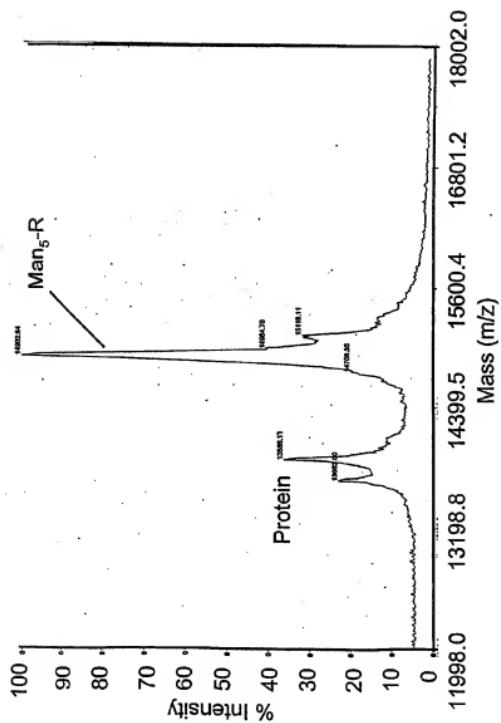


FIG. 183

489/498

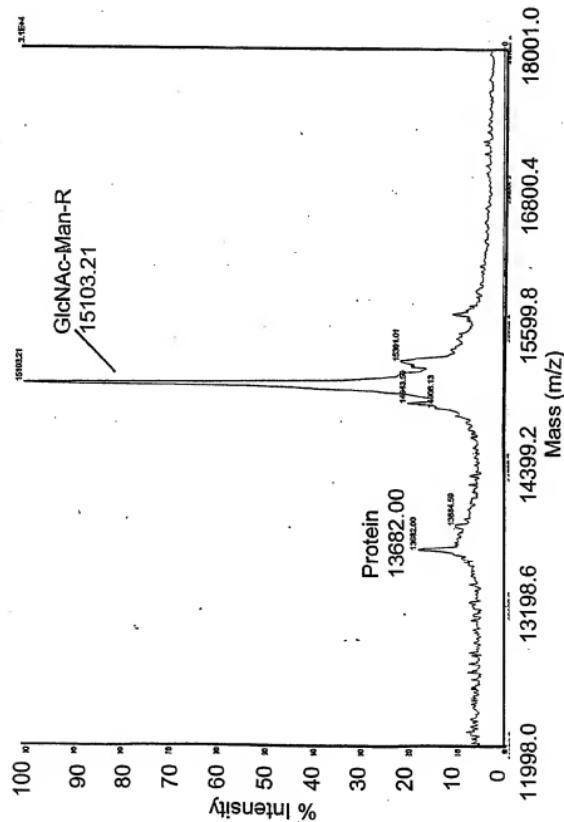


FIG. 184

490/498

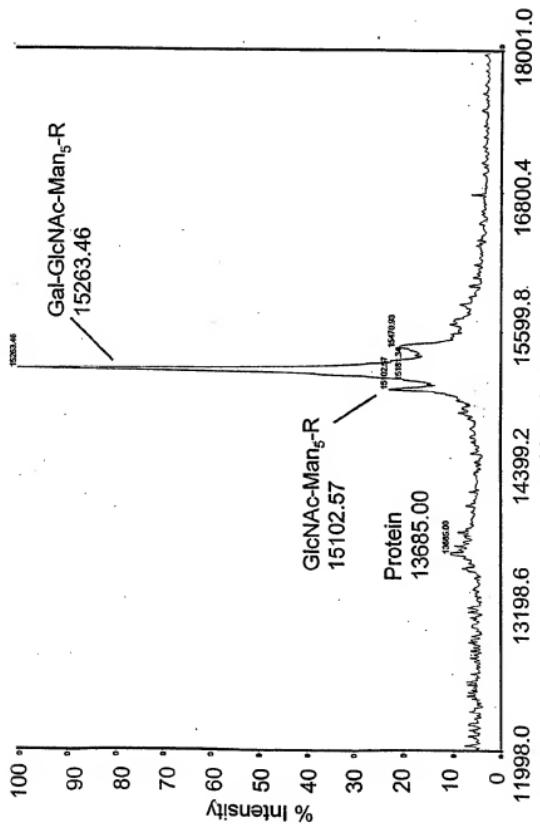


FIG. 185

491/498

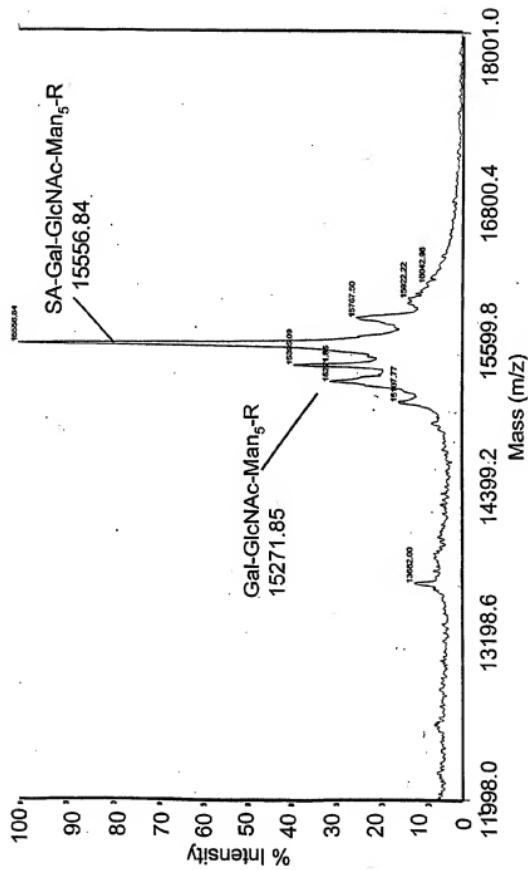


FIG. 186

492/498

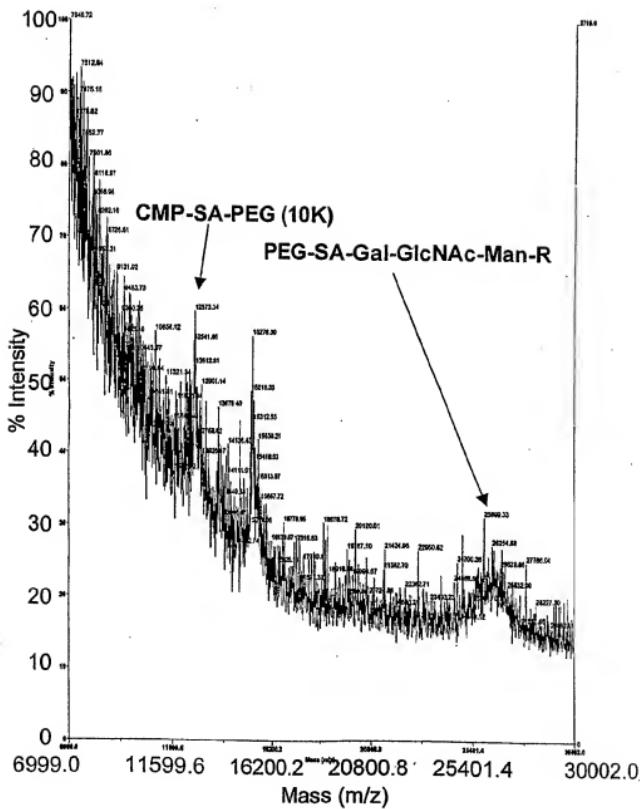


FIG. 187A

493/498

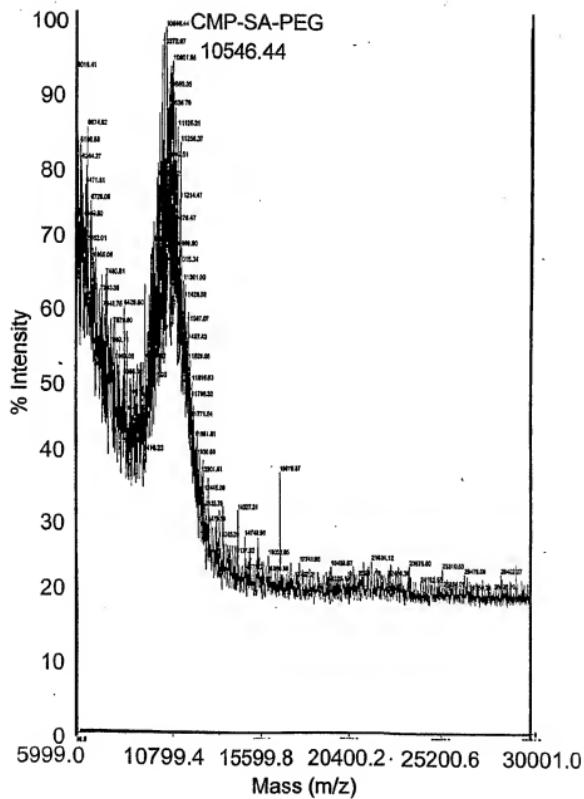
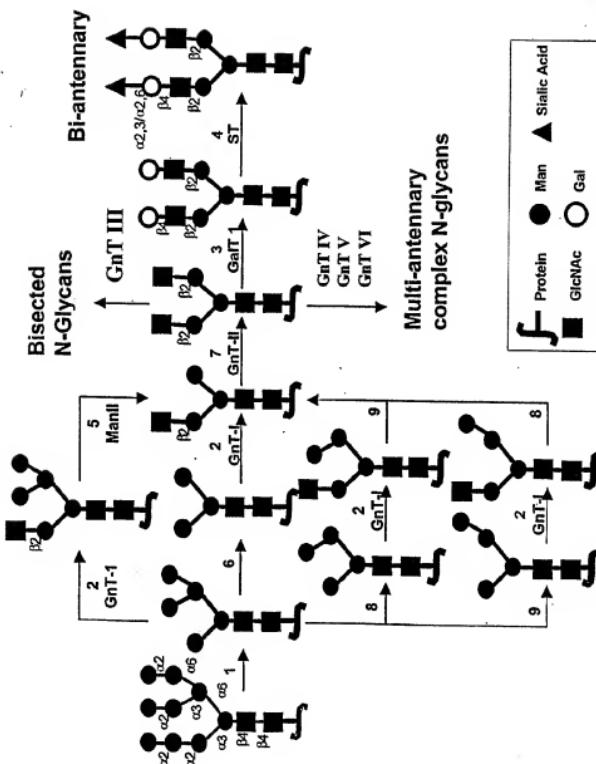


FIG. 187B

494/498

FIG. 188



495/498

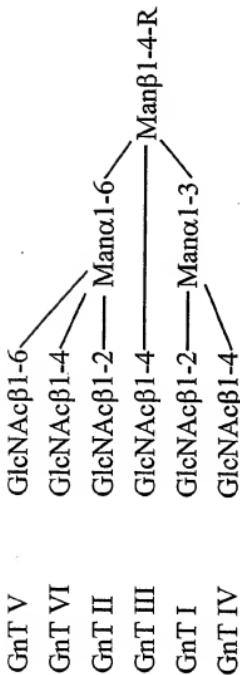


FIG. 189

496/498

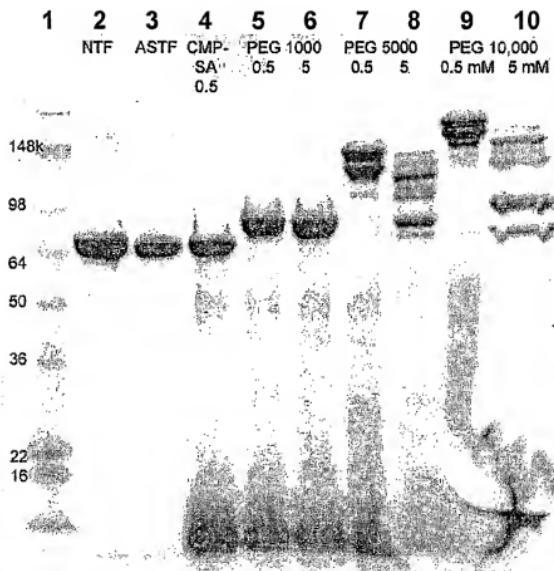


FIG. 190

497/498

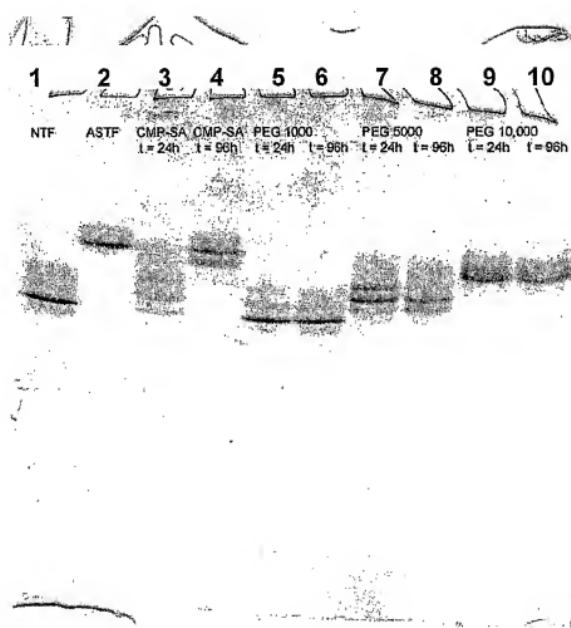
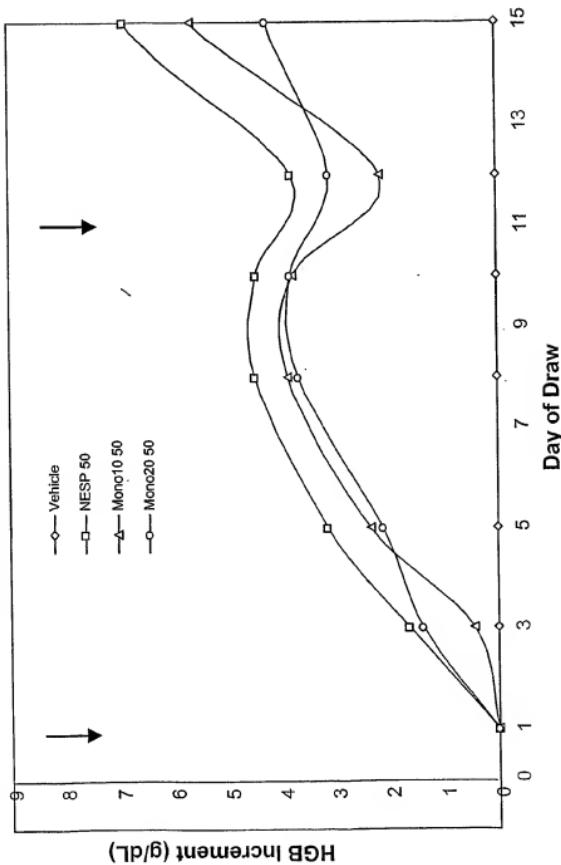


FIG. 191

498/498

Fig. 192 Hemoglobin response in rats



## SEQUENCE LISTING

<110> Neose Technologies, Inc.  
DeFrees, Shawn  
Zopf, David  
Bayer, Robert  
Hakes, David  
Chen, Xi  
Bowe, Caryne

<120> ERYTHROPOIETIN: REMODELING AND GLYCOCOCONJUGATION OF  
ERYTHROPOIETIN

<130> 040853-01-5083WO

<150> PCT/US02/32263  
<151> 2002-10-09

<150> US 10/287,994  
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 Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val  
 35 40 45  
 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
 50 55 60  
 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
 65 70 75 80  
 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
 85 90 95  
 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
 100 105 110  
 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
 115 120 125  
 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
 130 135 140  
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Gly Ser Arg Arg Thr Leu Met Leu Ala Gln Met Arg Arg Ile Ser  
 35 40 45

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu  
 50 55 60

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His  
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Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser

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Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys			
130	135	140	
Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro			
145	150	155	160
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Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu  
 50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile  
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Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser  
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Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
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Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser  
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Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile						
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Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Ala						
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Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile						
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 Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr  
 260 265 270  
 Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln  
 275 280 285  
 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg  
 290 295 300  
 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser  
 305 310 315 320  
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met  
 325 330 335  
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser  
 340 345 350  
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala  
 355 360 365  
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly  
 370 375 380  
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val  
 385 390 395 400  
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr  
 405 410 415  
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu  
 420 425 430  
 Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro  
 435 440  
 <210> 9  
 <211> 1437  
 <212> DNA  
 <213> Homo sapiens  
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 ggatatctac tcagtgtcga atgtacagg ttttcttgatc atgaaaacgc caacaaaattt 120

ctgaatccgc	caaagaggta	taattcaggta	aaatggaga	agtttgttca	agggaac	180
gagagagaata	gtatggaga	aaagtgttagt	tttgaagaac	cacgagaagt	ttttgaaaac	240
actgaaaaga	caactgaatt	ttggaagcag	tatgttgatg	gagatcagt	tgagtccaat	300
ccatgtttaa	atggcgccag	ttgcaaggat	gacattaatt	cctatgaatg	ttgggttccc	360
tttggatttgc	aaggaaagaa	ctgtgaatta	gatgtacat	gtaacattaa	gaatggcaga	420
tgcgagcagt	tttgtaaaaa	tagtgcgtat	aacaagggtgg	tttgcctctg	tactgaggg	480
tatcgacttgc	cagaaaacca	gaagtccgt	gaaccaggcag	tgcattttcc	atgtggaaga	540
gtttctgttt	cacaaaacttc	taagctcacc	cgtgtcgagg	ctgttttcc	tgtatggac	600
tatgtaaatc	ctactgaagc	tggataaccatt	ttggataaca	tcactcaagg	caccaatca	660
ttaatgact	tcactcggt	tgttggtgga	gaagatgcca	aaccaggta	attcccttgg	720
caggttgttt	tgaatggtaa	agttgtatqca	ttctgtggag	gctcttatcg	taatgaaaaa	780
tggattgtaa	ctgtcgccca	ctgtgttgaa	actgtgttta	aaattacagt	tgtcgaggt	840
gaacataata	ttgaggagac	agacataca	gagaaaaaagc	gaaatgtat	tgcgaaatt	900
attoctcacc	acaactcaa	tcagacttatt	aataagtaca	accatgacat	tgcccttctg	960
gaactggacg	aacccttagt	ctaaacacgc	tacggttacac	ctatgtcat	tgctgacaaag	1020
gaatacacga	acatcttct	caaattttgga	tctggctat	taagtggctg	ggcaagagtc	1080
ttccacaaag	ggagatcagc	tttagttctt	cagtagcccta	gagttccact	tgttgaccga	1140
gccacatgtc	ttcgatctac	aaagttcacc	atctataaca	acatgttctg	tgctggcttc	1200
catgaaggag	gtagagattc	atgtcaagga	gatagtgggg	gaccctatgt	tactgaagtg	1260
gaagggacca	gtttcttaac	tggatttatt	agctggggtg	aagagtgtgc	aatgaaaggc	1320
aaatatggaa	tataatcaa	ggtatcccg	tatgtcaact	ggattaagga	aaaaacaaag	1380
ctcacttaat	gaaagatgg	tttccaagg	taattcattt	gaattgaaa	ttaacag	1437
<210>	10					
<211>	462					
<212>	PRT					
<213>	Homo sapiens					

<400> 10  
Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr  
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu  
                  20                         25                         30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn  
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys

50	55	60	
Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn			
65	70	75	80
Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln			
85	90	95	
Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile			
100	105	110	
Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys			
115	120	125	
Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe			
130	135	140	
Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly			
145	150	155	160
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe			
165	170	175	
Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala			
180	185	190	
Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu			
195	200	205	
Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe			
210	215	220	
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp			
225	230	235	240
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile			
245	250	255	
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly			
260	265	270	
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu			
275	280	285	
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His			
290	295	300	
Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu			
305	310	315	320
Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys			
325	330	335	
Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly			
340	345	350	
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu			
355	360	365	
Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu			
370	375	380	

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe  
 385 390 395 400

His Glu Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His  
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp  
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val  
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr  
 450 455 460

<210> 11  
<211> 603  
<212> DNA  
<213> Homo sapiens

<400> 11  
atggattact acagaaaata tgcagctatac tttctggtca cattgtcggt gtttctgcat 60  
gttctccatt ccgctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccca 120  
ttcttcctcc agccgggtgc cccaaatactt cagtgcatgg gctgctgctt ctcttagagca 180  
tatcccactc cactaaggtc caagaagacg atgttggtcc aaaaagaacgt cacctcagag 240  
tccacttggt gtgttagctaa atcatataac agggtcacag taatgggggg tttcaaagtg 300  
gagaacceaca cggcgtggca ctgcagtaact tgttattata acaaatttta aatgttttac 360  
caagtgtgt ctgtatgact gctgattttc tggaatggaa attaagttt ttttagtggtt 420  
atggctttgt gagataaaac tctcccttcc cttaccatac cacttgaca cgcttcaagg 480  
atatactgc gctttactgc cttecccttcc atcctacagt acaaattcaga gtcttagttct 540  
tttcatttgg aatgaataca gcattaagct tgttccactg caaataaagc cttttaaatc 600  
atc 603

<210> 12  
<211> 116  
<212> PRT  
<213> Homo sapiens

<400> 12  
Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser  
1 5 10 15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro  
20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro  
35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro  
50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu			
65	70	75	80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly		
85	90	95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr		
100	105	110

Tyr His Lys Ser  
115

<210> 13

<211> 390

<212> DNA

<213> Homo sapiens

<400> 13

atgaagacac tccagttttt ctccctttc tggtgctgga aagcaatctg ctgcaatagc	60
--	----

tgtgagctga ccaacatcac cattgcaata gagaagaag aatgtcggtt ctgcataaggc	120
---	-----

atcaacacca cttgggtgtgc tggctactgc tacaccagg atctgggtta taaggaccca	180
---	-----

gccaggccca aaatccgaa aacatgtacc ttcaaggaa tggtatatga aacagtggaa	240
---	-----

gtgcccggct gtgctcacca tgcagattcc ttgtatacat acccagtggc cacccagtgt	300
---	-----

cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcc gggccccagc	360
--	-----

tactgtctt ttgggtgaaat gaaagaataa	390
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<210> 14

<211> 129

<212> PRT

<213> Homo sapiens

<400> 14

Met Lys Thr Leu Gln Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile			
1	5	10	15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys		
20	25	30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly		
35	40	45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys		
50	55	60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg			
65	70	75	80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val		
85	90	95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys		
100	105	110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys

115

120

125

Glu

&lt;210&gt; 15

&lt;211&gt; 1342

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

cccgaggccg gaccggggcc accggccccg ctctgtcccg acacccgcgc ccctggacag 60

ccgcctctc ctccaggccc gtggggctgg ccctgcaccc cggagttcc cgggatgagg 120

gccccgggtg tggcacccg ggcgcgccca ggtcgcttag ggaccccgcc caggcgccga 180

gtgggggtg cacgaatgtc ctgcctggc gtggcttctc ctgtccctgc tgtcgctccc 240

tctgggcctc ccagtccctgg ggcgcacc acgcctcatc tgtgacagcc gagtcctgg 300

gaggtaactc ttggaggcca aggaggcga gaatatcag acgggctgtg ctgaacactg 360

cagcttgaat gagaatatca ctgtcccca caccaaagt aatttctatg cctgaaagag 420

gtggagggtc gggcagcagg cctgagaagt ctggcagggc ctggccctgc tgtcgaaagc 480

tgtccctgcgg ggcgcaggccc tgggggtcaa ctctccca cctgaggccgc ccctgcagct 540

gcacgtgttat aaaggccgtca gtggcccttc cgcgcctacc actctgttc gggctctgcg 600

agccccagaag gaagccatct cccctccaga tgcggccctca gctgctccac tccgaacaat 660

caactgtgtac aatttccca aacttcccg agtctactcc aatttctcc gggaaagct 720

gaagctgtac acaggggagg octgcaggac agggacaga tgaccaggtg tgtccacactg 780

ggcatatcca ccaccccttccat caccacatt gttgtgccta caccctcccc cggccactcc 840

gaaccccggtc gaggggctct cagtcagecg ccacgcgttc ccatggacac tccagtgcga 900

gcaatgacat ctcaggggcc agaggaactg tccagagagc aactctgaga tctaaggatg 960

tcacaggggc aacttggggg cccagagcag gaagcattca gagagcagct taaaactcag 1020

ggacagagcc atgctggaa gacgcctgtc ctcactcgcc accctgaaa atttgatgcc 1080

aggcacacgt ttggaggcga ttacactgtt ttgcacacta ccatcaggga caggatgacc 1140

tggagaacctt aggtggcaag ctgtgacttc tccaggcttc acgggcatgg gcaactccctt 1200

ggtgccaaaga gcccccttga caccgggggtg gtgggaacca tgaagacagg atgggggtcg 1260

gcctctggct ctcattgggtt ccaagtttg tgtattcttc aacctcattt acaagaactg 1320

aaaccaccaa aaaaaaaaaaa aa 1342

&lt;210&gt; 16

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<400> 16  
 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu  
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu  
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu  
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu  
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu  
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser  
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly  
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu  
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile  
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu  
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
 180 185 190

Arg

<210> 17  
 <211> 435  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 atgtggctgc agagectgct gctcttggc actgtggcct gcagcatctc tgcacccggc 60  
 cgctcgccca gccccagcac gcagccctgg gagcatgtga atgcccattca ggaggcccg 120  
 cgttcctctga acctggatag agacaactgtc gtctggatgtc atgaaacagt agaagtcttc 180  
 tcagaaatgt ttgacactcca ggagccgacc tgcctacaga cccgcctgga gctgtacaag 240  
 caggccctgc gggcagccct cacaagctc aaggcccccgt tgaccatgtatgcaccc 300  
 tacaaggcgc actggccctcc aaccccgaa atttctgttgc caacccagat tatcacctt 360  
 gaaagttca aagagaacct gaaggacttt ctgttgtca tcccctttgc ctgtggag 420



&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu	1	5	10	15
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Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu	20	25	30
---	----	----	----

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn	35	40	45
---	----	----	----

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp	50	55	60
---	----	----	----

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe	65	70	75	80
---	----	----	----	----

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile	85	90	95
---	----	----	----

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg	100	105	110
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Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val	115	120	125
---	-----	-----	-----

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser	130	135	140
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Pro Ala Ala Lys Thr Gly Lys Arg Ser Gln Met Leu Phe Arg	145	150	155	160
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Gly Arg Arg Ala Ser Gln	165
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&lt;210&gt; 21

&lt;211&gt; 1352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

ctgggacagt gaatcgacaa tgccgttctc tgcgtcggtgg ggcattctcc tgctggcagg	60
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cctgtgtcgc ctgggtccctg tctccctggc tgaggatccc cagggagatg ctggcccaagaa	120
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gacagataca tccccaccatg atcaggatcca cccaaaccttc aacaagatca ccccaaacct	180
--	-----

ggctgtggatc gccttcagcc tataccgcga gctggcacac cagtccaaaca gcaccaataat	240
--	-----

cttttttctcc caagtqaqca tcgtatacqg ctttgcataatg ctctccctgg ggaccaaggc	300
--	-----

tgcacactcac gatgaaatcc tggaggggctt gaatttcaac ctcacggaga ttccggaggc	360
---	-----

tcatgatccat gaaggcttcc aggaactctt cgcgtaccctt aaccagccag acagccagct	420
---	-----

ccagctgacc accggcaatg gcctgttcc cagcgaggcc ctgaaatgtt tggataatgtt	480
---	-----

tttggaggat gttaaaaatgttgtaccactc agaaggcttc actgtcaact tcggggacac	540
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cgaagaggcc	aagaacaga	tcaacgatta	cgtggagaag	ggtactcaag	ggaaaattgt	600
ggatttgtc	aaggagctt	acagagacac	agttttgtc	ctggtaatt	acatcttctt	660
taaaggccaa	tgggagagac	ccttgaagt	caaggacacc	gaggaagagg	acttccacgt	720
ggaccaggtg	accacogtga	aggtgcctat	gatgaagcgt	ttaggcatgt	ttaacatcca	780
gcactgtaa	aagctgtcca	gctgggtgct	gctgtgaa	tacctggca	atgccaccgc	840
catcttc	ctgcgtat	agggaaact	acagcacctg	gaaaatgaac	tcacccacga	900
tatcatcacc	aagttcctgg	aaaatgaaga	cagaaggct	gccagcttac	atttacccaa	960
actgtccatt	actggAACCT	atgatgtaa	gagcgtcctg	ggtaactgg	gcatcaactaa	1020
ggtttc	aatggggctg	acctctccgg	ggtcacagag	gaggcacccc	tgaagctctc	1080
caaggccgtg	cataaggctg	tgctgaccat	cgacyagaaa	gggactgaag	ctgctggggc	1140
catgtttta	gaggccatac	ccatgtctat	cccccccgag	gtcaagtca	acaaaccctt	1200
tgtcttcta	atgattgaac	aaaataccaa	gtctccctc	ttcatggaa	aagtggtaa	1260
tccacccaa	aaataactgc	ctctcgctcc	tcaacccctc	ccctccatcc	ctggccccct	1320
ccctggatga	cattaaagaa	gggttgagct	gg			1352

&lt;210&gt; 22

&lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

Met	Pro	Ser	Ser	Val	Ser	Trp	Gly	Ile	Leu	Leu	Leu	Ala	Gly	Leu	Cys
1						5			10					15	

Cys	Leu	Val	Pro	Val	Ser	Leu	Ala	Glu	Asp	Pro	Gln	Gly	Asp	Ala	Ala
			20					25					30		

Gln	Lys	Thr	Asp	Thr	Ser	His	His	Asp	Gln	Asp	His	Pro	Thr	Phe	Asn
	35					40					45				

Lys	Ile	Thr	Pro	Asn	Leu	Ala	Glu	Phe	Ala	Phe	Ser	Leu	Tyr	Arg	Gln
	50					55					60				

Leu	Ala	His	Gln	Ser	Asn	Ser	Thr	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser
	65							70			75			80	

Ile	Ala	Thr	Ala	Phe	Ala	Met	Leu	Ser	Leu	Gly	Thr	Lys	Ala	Asp	Thr
			85					90				95			

His	Asp	Glu	Ile	Leu	Glu	Gly	Leu	Asn	Phe	Asn	Leu	Thr	Glu	Ile	Pro
	100							105				110			

Glu	Ala	Gln	Ile	His	Glu	Gly	Phe	Gln	Glu	Leu	Leu	Arg	Thr	Leu	Asn
	115							120				125			

Gln	Pro	Asp	Ser	Gln	Leu	Gln	Leu	Thr	Thr	Gly	Asn	Gly	Leu	Phe	Leu
	130							135			140				

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys  
 145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu  
 165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys  
 180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu  
 195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
 210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val  
 225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys  
 245 250 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala  
 260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu  
 275 280 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp  
 290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr  
 305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
 325 330 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys  
 340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly  
 355 360 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile  
 370 375 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu  
 385 390 395 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr  
 405 410 415

Gln Lys

<210> 23

<211> 2004

<212> DNA

<213> Homo sapiens

<400> 23  
gcttaacctag tgcctatagc taaggcaggt acctgcattcc ttgttttgtt ttagtggttc 60



tagaaaaaga tcagtaagcc ccagtgtccc cccagcccc atgcttatgt gaacatgcgc 1980  
tgtgtgtcgc ttgctttgga aact 2004

<210> 24  
<211> 536  
<212> PRT  
<213> Homo sapiens

<400> 24  
Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser  
1 5 10 15  
Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Gln  
20 25 30  
Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe  
35 40 45  
Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser  
50 55 60  
Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu  
65 70 75 80  
Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln  
85 90 95  
Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
100 105 110  
Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala  
115 120 125  
Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu  
130 135 140  
Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val  
145 150 155 160  
Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp  
165 170 175  
Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp  
180 185 190  
Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln  
195 200 205  
Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu  
210 215 220  
Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro  
225 230 235 240  
Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu  
245 250 255  
Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu  
260 265 270

Asn	Glu	Phe	Ser	Ala	Gly	Leu	Leu	Ser	Gly	Tyr	Pro	Phe	Gln	Cys	Leu
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Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg  
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val  
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile  
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln  
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser  
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser  
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp  
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu  
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser  
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile  
 180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr  
 195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly  
 210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp  
 225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr  
 245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val  
 260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile  
 275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser  
 290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met  
 305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His  
 325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro  
 340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp  
 355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser  
 370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr  
 385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro  
 405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn  
 420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met  
 435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu  
 450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu  
 465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro  
 485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys

500	505	510
Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe		
515	520	525
Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp		
530	535	540
Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg		
545	550	555
Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu		
565	570	575
Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val		
580	585	590
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu		
595	600	605
Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp		
610	615	620
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val		
625	630	635
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp		
645	650	655
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe		
660	665	670
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr		
675	680	685
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro		
690	695	700
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly		
705	710	715
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp		
725	730	735
Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys		
740	745	750
Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg		
755	760	765
Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp		
770	775	780
Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys		
785	790	795
Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser		
805	810	815
Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr		
820	825	830

Glu	Thr	Phe	Ser	Asp	Asp	Pro	Ser	Pro	Gly	Ala	Ile	Asp	Ser	Asn	Asn
835															845
Ser	Leu	Ser	Glu	Met	Thr	His	Phe	Arg	Pro	Gln	Leu	His	His	Ser	Gly
850															860
Asp	Met	Val	Phe	Thr	Pro	Glu	Ser	Gly	Leu	Gln	Leu	Arg	Leu	Asn	Glu
865															880
Lys	Leu	Gly	Thr	Thr	Ala	Ala	Thr	Glu	Leu	Lys	Lys	Leu	Asp	Phe	Lys
885															895
Val	Ser	Ser	Thr	Ser	Asn	Asn	Leu	Ile	Ser	Thr	Ile	Pro	Ser	Asp	Asn
900															910
Leu	Ala	Ala	Gly	Thr	Asp	Asn	Thr	Ser	Ser	Leu	Gly	Pro	Pro	Ser	Met
915															925
Pro	Val	His	Tyr	Asp	Ser	Gln	Leu	Asp	Thr	Thr	Leu	Phe	Gly	Lys	Lys
930															940
Ser	Ser	Pro	Leu	Thr	Glu	Ser	Gly	Gly	Pro	Leu	Ser	Leu	Ser	Glu	Glu
945															960
Asn	Asn	Asp	Ser	Lys	Leu	Leu	Glu	Ser	Gly	Leu	Met	Asn	Ser	Gln	Glu
965															975
Ser	Ser	Trp	Gly	Lys	Asn	Val	Ser	Ser	Thr	Glu	Ser	Gly	Arg	Leu	Phe
980															990
Lys	Gly	Lys	Arg	Ala	His	Gly	Pro	Ala	Leu	Leu	Thr	Lys	Asp	Asn	Ala
995															1005
Leu	Phe	Lys	Val	Ser	Ile	Ser	Leu	Leu	Lys	Thr	Asn	Lys	Thr	Ser	
1010															1020
Asn	Asn	Ser	Ala	Thr	Asn	Arg	Lys	Thr	His	Ile	Asp	Gly	Pro	Ser	
1025															1035
Leu	Leu	Ile	Glu	Asn	Ser	Pro	Ser	Val	Trp	Gln	Asn	Ile	Leu	Glu	
1040															1050
Ser	Asp	Thr	Glu	Phe	Lys	Lys	Val	Thr	Pro	Leu	Ile	His	Asp	Arg	
1055															1065
Met	Leu	Met	Asp	Lys	Asn	Ala	Thr	Ala	Leu	Arg	Leu	Asn	His	Met	
1070															1080
Ser	Asn	Lys	Thr	Thr	Ser	Ser	Lys	Asn	Met	Glu	Met	Val	Gln	Gln	
1085															1095
Lys	Lys	Glu	Gly	Pro	Ile	Pro	Pro	Asp	Ala	Gln	Asn	Pro	Asp	Met	
1100															1110
Ser	Phe	Phe	Lys	Met	Leu	Phe	Leu	Pro	Glu	Ser	Ala	Arg	Trp	Ile	
1115															1125
Gln	Arg	Thr	His	Gly	Lys	Asn	Ser	Leu	Asn	Ser	Gly	Gln	Gly	Pro	
1130															1140

Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu  
 1145 1150 1155  
 Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys  
 1160 1165 1170  
 Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe Pro  
 1175 1180 1185  
 Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu  
 1190 1195 1200  
 Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu  
 1205 1210 1215  
 Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile  
 1220 1225 1230  
 His Thr Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu  
 1235 1240 1245  
 Leu Ser Thr Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr  
 1250 1255 1260  
 Ala Pro Val Leu Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn  
 1265 1270 1275  
 Arg Thr Lys Lys His Thr Ala His Phe Ser Lys Lys Gly Glu Glu  
 1280 1285 1290  
 Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu  
 1295 1300 1305  
 Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln  
 1310 1315 1320  
 Asn Phe Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg  
 1325 1330 1335  
 Leu Pro Leu Glu Glu Thr Glu Leu Glu Lys Arg Ile Ile Val Asp  
 1340 1345 1350  
 Asp Thr Ser Thr Gln Trp Ser Lys Asn Met Lys His Leu Thr Pro  
 1355 1360 1365  
 Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu Lys Gly Ala  
 1370 1375 1380  
 Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser  
 1385 1390 1395  
 Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser  
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 Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe  
 1415 1420 1425  
 Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys  
 1430 1435 1440  
 Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys

1445	1450	1455
Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly		
1460	1465	1470
Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser		
1475	1480	1485
Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp		
1490	1495	1500
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His		
1505	1510	1515
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser		
1520	1525	1530
Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr		
1535	1540	1545
Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val		
1550	1555	1560
Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser		
1565	1570	1575
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln		
1580	1585	1590
Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys		
1595	1600	1605
Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys		
1610	1615	1620
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys		
1625	1630	1635
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg		
1640	1645	1650
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu		
1655	1660	1665
Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr		
1670	1675	1680
Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile		
1685	1690	1695
Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys		
1700	1705	1710
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr		
1715	1720	1725
Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser		
1730	1735	1740
Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr		
1745	1750	1755

Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu
1760						1765					1770			
His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	Glu	Asp
1775						1780					1785			
Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser
1790						1795					1800			
Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly
1805						1810					1815			
Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr
1820						1825					1830			
Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu
1835						1840					1845			
Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu
1850						1855					1860			
Lys	Asp	Val	His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His
1865						1870					1875			
Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln
1880						1885					1890			
Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp
1895						1900					1905			
Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn
1910						1915					1920			
Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe	Lys	Glu	Asn	Tyr	Arg	Phe	His
1925						1930					1935			
Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	Thr	Leu	Pro	Gly	Leu	Val	Met
1940						1945					1950			
Ala	Gln	Asp	Gln	Arg	Ile	Arg	Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser
1955						1960					1965			
Asn	Glu	Asn	Ile	His	Ser	Ile	His	Phe	Ser	Gly	His	Val	Phe	Thr
1970						1975					1980			
Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met	Ala	Leu	Tyr	Asn	Leu	Tyr
1985						1990					1995			
Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met	Leu	Pro	Ser	Lys	Ala	Gly
2000						2005					2010			
Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly	Glu	His	Leu	His	Ala	Gly
2015						2020					2025			
Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys	Gln	Thr	Pro
2030						2035					2040			
Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	Thr	Ala
2045						2050					2055			

Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His  
 2060 2065 2070

Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser  
 2075 2080 2085

Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile  
 2090 2095 2100

Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser  
 2105 2110 2115

Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr  
 2120 2125 2130

Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn  
 2135 2140 2145

Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile  
 2150 2155 2160

Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg  
 2165 2170 2175

Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys  
 2180 2185 2190

Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln  
 2195 2200 2205

Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser  
 2210 2215 2220

Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp  
 2225 2230 2235

Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe  
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Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys  
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Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser  
 2270 2275 2280

Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys  
 2285 2290 2295

Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val  
 2300 2305 2310

Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His  
 2315 2320 2325

Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu  
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Gly Cys Glu Ala Gln Asp Leu Tyr  
 2345 2350

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cggctcaagag aatactatga ccagacagct cagatgtgt gcagcaaatg ctgcggggc 180  
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acgttccacgt ccccccacccg ggtatggcc ccaaggggcag tacacttacc ccagccagg 660  
tccacacat cccaaacacac gcagccaact ccagaacccca gcactgtcc aagcacctcc 720  
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ccagttggac tgatttgtgg tggacagcc ttgggtctac taataatagg agtgtgtgaac 840  
tgtgtcatca tgaccaggta gaaaaaaaga cccttgc tgcagagaga agccaagggt 900  
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<400> 32

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Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
 85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
 100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser  
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly  
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly  
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys  
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro  
 290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser

325	330	335
Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly		
340	345	350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser		
355	360	365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile		
370	375	380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln		
385	390	395

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro		
405	410	415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser		
420	425	430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro		
435	440	445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser		
450	455	460

<210> 33

<211> 1475

<212> DNA

<213> Homo sapiens

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taaaatggagg aacatgtgtc tccaacaagt acttctccaa catttcactgg tgcaactgcc	240
caaagaatt cggaggggcag cactgtgaaa tagataagtcc aaaaacctgc tatgagggga	300
atggtaacctt ttaccggaga aaggccagca ctgacacccat gggccggccc tgcctgcct	360
ggaaactctgc cactgtcctt cagcaaacgt accatggccca cagatctgtat gctttcagc	420
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atgtgcagggt gggcttaaag cogcttgcc aagagtgcat ggtgcatgc tgccgcagatg	540
aaaaaaagcc ctcctctctt ccagaagaat taaaatttca gtgtggccaa aagactctga	600
ggcccccgtt taagatttatt gggggagaat tcaccacccat cgagaaccag ccctgggtttg	660
cggccatcta caggaggcac cgggggggtt ctgttcaccta cgtgtgtggaa ggcagccctca	720
tcagcccttg ctgggtgtatc agcgcacac actgtttcat tgattaccca aagaaggagg	780
actacatcgat ctacctgggt cgctcaaggc ttaactccaa cacgcaaggg gagatgaagt	840
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acgacattgc ttgtctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga 960  
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 <211> 431  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 34  
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 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
 35 40 45  
  
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
 50 55 60  
  
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly  
 65 70 75 80  
  
 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser  
 85 90 95  
  
 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
 100 105 110  
  
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
 115 120 125  
  
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
 130 135 140  
  
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
 145 150 155 160  
  
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
 165 170 175  
  
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp

180	185	190
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val		
195	200	205
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His		
210	215	220
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly		
225	230	235
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val		
245	250	255
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His		
260	265	270
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys		
275	280	285
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr		
290	295	300
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys		
305	310	315
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val		
325	330	335
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly		
340	345	350
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys		
355	360	365
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu		
370	375	380
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys		
385	390	395
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu		
405	410	415
Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu		
420	425	430
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<211> 107		
<212> PRT		
<213> Mus musculus		
<400> 35		
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15		
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20	25	30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile		
35	40	45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 36

<211> 120

<212> PRT

<213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr  
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 37

<211> 120

<212> PRT

<213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
 20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu  
 35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser  
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala  
100 105 110

Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 38

<211> 106

<212> PRT

<213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met  
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr  
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp  
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr  
85 90 95

Phe Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 39

<211> 1039

<212> DNA

<213> Homo sapiens

<400> 39

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cattctcgtc atctctgagg acatcacat catctcgagg tgaggggcat gaagctgtgt 180

ggggcgctgc tggcaactgc ggcctactg cagggggcgc tgccctgaa gatgcagcc 240

ttcaacatcc agacattgg ggagacccaag atgtccaatg ccaccctcggt cagctacattt 300

gtgcagatcc tgagccgcta tgacatcgcc ctgggtcagg aggtcagaga cagccacctg 360

actgccgtgg ggaagctgtt ggacaaacctc aatcaggatg caccagacac ctatcaactc 420

gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480

cctgaccagg	tgtctgcgg	ggacagctac	tactacgatg	atggctgcga	gccctgcggg	540
aacgacacct	tcaaccgaga	gccagccatt	gtcaggttct	tctcccggtt	cacagaggtc,	600
agggagtttgc	ccattgttcc	cctgcatgcg	gccccggggg	acgcagtagc	cgagatcgac	660
gtctctatg	acgtctaccc	ggatgtccaa	gagaatggg	gcttggagga	cgtcatgttg	720
atgggcact	tcaatgcggg	ctgcagctat	gtgagaccc	cccagtggtc	atccatccgc	780
ctgtggacaa	gccccaccc	ccagtggctg	atccccgaca	gcgctgacac	cacagctaca	840
cccacgact	gtgcctatga	caggatcg	gttgcaggga	tgcgtctccg	aggcgccgtt	900
gttccgact	cggcttcc	ctttaactc	caggctgc	atggcctgag	tgaccaactg	960
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cacaccagg	ttt	ttt	ttt	ttt	ttt	1039
<210>	40					
<211>	282					
<212>	PRT					
<213>	Homo sapiens					
Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu						
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Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr						
20	25	30				
Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val						
35	40	45				
Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp						
50	55	60				
Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp						
65	70	75	80			
Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn						
85	90	95				
Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser						
100	105	110				
Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn						
115	120	125				
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe						
130	135	140				
Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly						
145	150	155	160			
Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val						
165	170	175				
Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn						
180	185	190				

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
 195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
 210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
 225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
 245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
 260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys  
 275 280

<210> 41

<211> 678

<212> DNA

<213> Mus musculus

<400> 41  
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aatggttctc caaggcttct cataaaagtat gttctgtact ctatgtctgg gatcccttcc 180

aggttttagtgc gcaatggatc agggacatgt tttactctta gcatcaaacatgtggatct 240

gaagatattgc cagattatttc ctgtcaacaa agtcatagtc ggcatttcac gttcggtctcg 300

gggacaaattt tggaaataaa agaagtgaag cttggaggatc ctggaggaggatc 360

cctggaggatc ccatgaaactt ctcctgtgtt gcctctggat tcattttca taaccactgg 420

atgaactggg tccggccatc tccagagaag gggcttgatgc ggggtgtca aatttagatca 480

aaatcttata attctgcAAC acattatgcg gagttctgtgc aaggaggtt caccatctca 540

agagatgattt ccaaaatgc tgcgttacatc caaatgaccg acttaagaac tgaagacact 600

ggcggtttatc actgttccatc gaattactac ggttagtaccc acgactactg gggccaaggc 660

accactctca cagtctcc 678

<210> 42

<211> 226

<212> PRP

<213> Mus musculus

<400> 42  
 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly  
 1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser  
 20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile			
35	40	45	
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly			
50	55	60	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser			
65	70	75	80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe			
85	90	95	
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu			
100	105	110	
Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser			
115	120	125	
Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val			
130	135	140	
Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser			
145	150	155	160
Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg			
165	170	175	
Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met			
180	185	190	
Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn			
195	200	205	
Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr			
210	215	220	
Val Ser			
225			
<210> 43			
<211> 450			
<212> DNA			
<213> Homo sapiens			
<400> 43			
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tgaaccaaca cctgtgcggc tcacacctgg ttggaaatctt ctacactgttg tgccgggaaac	180		
gaggcttctt ctacacaccc aagacccggc gggagcaga ggacctgcag gtggggcagg	240		
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tgcagaacgcg tggcatttgtt gaacaatgtt gtaccaggcat ctgtccccctt taccagctgg	360		
agaactactg caactagacg cagcccgacg cgacgcccccc acccggccgcg tccctgcacccg	420		
agagagatgg aataaagccc ttgaaccagc	450		

<210> 44  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 44  
Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu  
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly  
20 25 30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe  
35 40 45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly  
50 55 60

Gln Val Glu Leu Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu  
65 70 75 80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys  
85 90 95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn  
100 105 110

<210> 45  
<211> 1203  
<212> DNA  
<213> Hepatitis B virus

<400> 45  
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cctctggat tcttccc当地 tcaccaggta gaccctgc当地 tcggagcc当地 ctcaaaca当地at 120  
ccagatggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggttaggagcg 180  
ggagacttc当地 ggc当地gggtt cacccacca cacggc当地tcc当地 ttttgggg当地 gagccctc当地ag 240  
gctcaggc当地 tattgacaaac agtgc当地agca ggc当地ctc当地 ctgttcc当地 caatggc当地ag 300  
tcaggaagac agc当地tactcc catctctcc当地 cctctaagag acagtcatcc tcaggccatg 360  
cagtggaaact ccacaacatt ccaccaactg ctgcttagatc ccagagttag gggc当地tat 420  
tttccctctgctg gtggctccag ttccgg当地aca gtaaaccctg ttccgactac tgc当地tcc当地accc 480  
atatcgctca local tttctcgag gactggggac cctgc当地ccgca acatggagag cacaacatca 540  
ggattccctag gacccctctg ctgttacag ggggg当地ttt tcttggtgac aagaatcc 600  
acaataccac agagtctaga ctctgtt当地ggg acttctctca attttctagg gggagcc 660  
acgtgtctg gccaatcc local gc当地tccccca acctccaatc actccaccaac ctcttgc当地ct 720  
ccatttgctc ctggatgtt ctggatgtt ctggccqgtt ttatcatatt ctcttctc当地at 780  
ctgtgtctat gcctcatcc ttgtt当地ggg ctcttggact accaaggat gttggccgtt 840

tgtcctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt 900  
 cctgctaaag gaacctctat gttccctct tggtgctgta caaaaccttc ggacggaaac 960  
 tgcacttcta ttccccatccc atcatectgg gtttcgccaa gatccctatg ggagtggcc 1020  
 tcagtcgggtt totectggct cagttacta gtgcatttg ttcatgtgtt cgcaagggtt 1080  
 tccccactg tttggcttc agttatatgg atgtatgtt attggggcc aagtctgtac 1140  
 aacatcttga gtccctttt acctctatta ccaattttct tttgtctttg ggtatacatt 1200  
 tga 1203

<210> 46  
<211> 400  
<212> PRT  
<213> Hepatitis B virus

<400> 46  
Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu  
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro  
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn  
35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly  
50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln  
65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser  
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu  
100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His  
115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly  
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro  
145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu  
165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly  
180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly  
210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro			
225	230	235	240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile		
245	250	255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu		
260	265	270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser		
275	280	285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly		
290	295	300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn			
305	310	315	320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu		
325	330	335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Ieu Val Pro		
340	345	350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val		
355	360	365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser		
370	375	380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile			
385	390	395	400

&lt;210&gt; 47

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 47		
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ccaaaccatt cccttatcca ggcctttta caacgcatttgc ctcgcggccc atcgctctgca		180
ccagctggcc tttgacacctt accaggagtt tgaagaagcc tatatccaa aggaacagaa		240
gtatccatcc ctgcagaacc cccagaccc cctctgtttc tcagatctta ttccgacacc		300
ctccaaacagg gaggaaacac aacagaatac caaccttagag ctgctccgca ttcctctgtt		360
gctcatccatcg tctgtggctgg agcccggtca gttcccttgg agtgtcttcg ccaacagcc		420
ggtgtacggc gcctctgaca gcaacgtcta tgacccctta aaggacctag aggaaggcat		480
ccaaacgctg atggggaggg tggaaatggc cagccccgg actggcaga tcttcaagca		540
gacttacagc aagttcgaca caaactcaca caacgtatgc gcactactca agaactacgg		600
gctgctctac tgcttcagga aggacatgga caaggtcgag acattcctgc gcategtgca		660

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 ctcggggatgt ccttcctctgg ccctggaaat tgccactcca gtggccacca gccttgtct 780  
 aataaaaatata agttgcata 799  
  
 <210> 48  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 48  
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 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu  
 20 25 30  
 Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln  
 35 40 45  
 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys  
 50 55 60  
 Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe  
 65 70 75 80  
 Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys  
 85 90 95  
 Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
 100 105 110  
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val  
 115 120 125  
 Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu  
 130 135 140  
 Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg  
 145 150 155 160  
 Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser  
 165 170 175  
 His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe  
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Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg

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Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly		
275	280	285
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu		
290	295	300
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro		
305	310	315
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu		
325	330	335
Gin Glu Trp Leu Asp Glu Leu Glu Lys Met Met Leu Val Val His Met		
340	345	350
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln		
355	360	365
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro		
370	375	380
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe		
385	390	395
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala		
405	410	415
Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val		
420	425	430
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro		
435	440	445
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys		
450	455	460
<210> 65 <211> 1962 <212> DNA <213> Homo sapiens		
<400> 65 atgcgtcccc tgcgcccccg cgccgcgcgtg ctggcgctcc tggcctcgct cctggccgcg cccccggtgg ccccgccgaa ggcccccacat ctgggtgcagg tggacgcggc ccgcgcgcgt tggccctgc ggcgcattctg gaggagcaca ggcttctgcc ccccgctgcc acacagccag	6	12
		18

gctgaccagt acgtcctca	ctgggaccag cagtc	aacc tcgcctatgt gggcgccgtc	240		
cctcaccccg	gcatcaagca	ggtccggacc cactggctgc	tggagcttgtt caccaccagg	300	
ggtccactg	gacggggcct	gagctacaac tt	acccacc tggacggta ctggac	360	
ctcaggaga	accagctct	cccagggttt gagctgtatgg	gcagcgcc	420	
actgacttt	aggacaagca	gcagggtttt gagtggaaagg	acttggctc	480	
aggagatata	tcggtagta	cg	gactggcg catgttcca	540	
aatgagccag	accaccaega	cttgacaa	cttgc	600	
tactacatg	cctgtcgga	gggtctcg	ccgc	ccgcagcc	660
cccgccgact	cctccacac	cccacccg	cgcc	ctggagg	720
tgccacacg	gtaccaactt	cttactggg	gaggcg	ggc tgccgtgg	780
ctccacagga	agggtgcgcg	cagtc	ccatctgg	cttgc	840
cagcagatcc	ggcagatctt	ccccaa	gttc	ccatccat	900
gaccgcgtt	tgggtgtt	ccgtccacag	ccgtgg	gggg cgacgt	960
atgggtgtt	aggcatcg	gcagcatcg	aac	ctgtcc	1020
ttccccatcg	cgtc	ctctg	ccatctgg	agcagg	1080
gogcagcga	cgtc	accgc	gttcc	ccatcc	1140
ctgttg	ccgc	gggtgt	ccatctgg	cgctgtgg	1200
ctctggcc	aagtgtc	ggccgg	gtc	ccatcc	1260
ctggccacg	cccaccc	ccagg	ccatcc	ccgcacgt	1320
tacgcg	acgacaccc	ccccc	ccatcc	ccgcgt	1380
cgccgg	ccccc	ggg	ccatcc	ccgcgt	1440
tgca	cccc	cccg	ccatcc	ccgcgt	1500
ttccgg	tgcc	gggg	ccatcc	ccgcgt	1560
ggccgg	tgac	cccg	ccatcc	ccgcgt	1620
tgtgcgc	ccgaga	cccg	ccatcc	ccgcgt	1680
caaggc	tgtttctgtt	ctgg	ccatcc	ccgcgt	1740
tacgagatcc	agttctctca	ggac	ccatcc	ccgcgt	1800
ac	tttgcgtt	ccatcc	ccatcc	ccgcgt	1860
cgac	ccatcc	ccatcc	ccatcc	ccgcgt	1920
gtcc	ctgtgc	caagagg	ccatcc	ccgcgt	1962

<210> 66  
 <211> 653  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 66  
 Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser  
 1 5 10 15  
 Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val  
 20 25 30  
 Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg  
 35 40 45  
 Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr  
 50 55 60  
 Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val  
 65 70 75 80  
 Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu  
 85 90 95  
 Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr  
 100 105 110  
 His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro  
 115 120 125  
 Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu  
 130 135 140  
 Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala  
 145 150 155 160  
 Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn  
 165 170 175  
 Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser  
 180 185 190  
 Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly  
 195 200 205  
 Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser  
 210 215 220  
 Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His  
 225 230 235 240  
 Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu  
 245 250 255  
 Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile  
 260 265 270  
 Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro  
 275 280 285  
 Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val

290	295	300
Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala		
305	310	315
Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn		
325	330	335
Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe		
340	345	350
Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg		
355	360	365
Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys		
370	375	380
Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln		
385	390	395
Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His		
405	410	415
Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp		
420	425	430
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala		
435	440	445
His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro		
450	455	460
Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu		
465	470	475
Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro		
485	490	495
Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala		
500	505	510
Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro		
515	520	525
Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro		
530	535	540
Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr		
545	550	555
Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys		
565	570	575
Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr		
580	585	590
Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser		
595	600	605
Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp		
610	615	620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu			
625	630	635	640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro	
645	650

&lt;210&gt; 67

&lt;211&gt; 1290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 67	
atgcaggctga ggaacccaga actacatctg ggctgcgcgc ttgcgttgc cttectggcc	60
ctcggtttctt gggacatccc tggggctaga gcactggaca atggattggc aaggacgcct	120
accatgggct ggctgcactg ggagcgcctt atgtgcaccc ttgactgcac ggaagagccca	180
gattcctgcac tcaagtggaaa gctcttcatg gagatggcag agtcatggt ctcagaaggc	240
tggaaaggatg cagggttatga gtacccctgc attgtatgtt gttggatggc tccccaaaga	300
gattcagaag gcagacttca ggcagacccct cagcgccttc ctcatggat tggccagctt	360
gctaattatg ttcacagcaa aggactgaag cttagggattt atgcagatgt tgaaataaaa	420
acctgcgcac gcttccctgg gagtttttgg tactacgaca ttgatgcacca gaccccttgc	480
gactggggag tagatctgtt aaaaattgtt gttgtttact gtgacagttt ggaaaattttt	540
gcagatgtt ataagcacat gtcccttgcc ctgaataggaa ctggcagaag cattgtgtac	600
tcctgtgtt ggcctcttta tatgtggccc tttccaaagc ccaattatac agaaatccga	660
cagtaactgcac atcactggcg aaattttgtt gacattgtat ttccctggaa aagtataaag	720
agtatcttgg actggacatc tttaaccag gagagaattt ttgatgttgc tggaccagg	780
ggttggaaatg acccagatata gttgtgtttt gcaactttt gcttcagctg gaatcagca	840
gttaactcaga tggccctctg ggctatcatg gctgtcttattcatgtc taatgaccc	900
cgacacatca gccctcaagc caaagctctc ctccaggata aggacgtaat tgccatcaat	960
caggacccct tggcagca agggttaccag cttagacagc gagacaacctt tgaagtgtgg	1020
gaacgacactc ttcaggctt agcctgggtt gtagctatg taaaccggca ggagattgtt	1080
ggacccctgtt ctataccat cgcaggctgtt ccctgggtt aaggagtggc ctgtatcc	1140
gcctgttca tcacacagct cttccctgtt aaaaggaage tagggttcta tgaatggact	1200
tcaaggtaa gaagtccacat aaatcccacca ggcactgtt tgcttcagct agaaaataaca	1260
atgcagatgtt cattaaaaga cttactttaa	1290

&lt;210&gt; 68

&lt;211&gt; 429

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<400> 68  
 Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu  
 1 5 10 15

Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu  
 20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu  
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile  
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly  
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met  
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg  
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly  
 115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly  
 130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala  
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser  
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn  
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met  
 195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
 210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys  
 225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val  
 245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn  
 260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala  
 275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser  
 290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn  
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala  
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Pro Arg Ser Tyr Thr Ile Ala  
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile  
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
 405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu  
 420 425

<210> 69

<211> 351

<212> DNA

<213> Homo sapiens

<400> 69

atggattact acagaaaata tgcagctate ttcttggta cattgtcggt gtttctgcat 60

gttctccatt ccgcctctga tgcgcaggat tgcccaaat gcacgcataa ggaaaaccca 120

tttttttccc agcccggtgc cccaaatactt cagtgcataa gctgcgtcct ctcttagaca 180

tatccccactc cactaaggtc caagaagacg atgttggtcc aaaagacgt cacctcagag 240

tccacttgtt gtgttagctaa atcatataac agggtcacag taatgggggg tttcaaagt 300

gagaaccaca cggcgtgcca ctgcgtact tgttattatc acaaattta a 351

<210> 70

<211> 116

<212> PRT

<213> Homo sapiens

<400> 70

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser  
 1 5 10 15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro  
 20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro  
 35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro  
 50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu  
 65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly  
 85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr  
 100 105 110

Tyr His Lys Ser  
 115

<210> 71  
<211> 498  
<212> DNA  
<213> Homo sapiens

<400> 71  
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tccaaggagc cgcttcggcc acgggtccgc cccatcaatg ccaccctggc tggggagaag 120  
gaggggctgcc cggtgtcat caccgtcaac accaccatct gtggccgcta ctggccccacc 180  
atgaccccgcg tgctgcaggg ggtcctgcgg gcccctgcctc aggtggtgtg caactaccgc 240  
gtatgtgcgt tcgagttccat cccggctccat ggctgcggcc gccggcgtgaa ccccggtggc 300  
tcctacccgc tggctctca tagtcaatgt gcaacttcgc gccgcagcac cactgactgc 360  
gggggtccca aggaccaccc ctggacctgt gatgacccccc gcttccagga ctccctttcc 420  
tcaaaggccc ctccccccag cttccaagc ccattccgac tcccggggcc ctggacacc 480  
ccgatccccc cacaataa 498

<210> 72  
<211> 165  
<212> PRT  
<213> Homo sapiens

<400> 72  
Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly  
1 5 10 15

Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile  
20 25 30

Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr  
35 40 45

Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val  
50 55 60

Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg  
65 70 75 80

Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val  
85 90 95

Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu  
100 105 110

Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu

115	120	T25
Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Lys Ala Pro		
130	135	140
Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr		
145	150	155
Pro Ile Leu Pro Gln		
165		
<210> 73		
<211> 165		
<212> PRT		
<213> Homo sapiens		
<400> 73		
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu		
1	5	10
15		
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His		
20	25	30
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe		
35	40	45
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp		
50	55	60
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu		
65	70	75
80		
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp		
85	90	95
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu		
100	105	110
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala		
115	120	125
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val		
130	135	140
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala		
145	150	155
160		
Cys Arg Thr Gly Asp		
165		
<210> 74		
<211> 588		
<212> DNA		
<213> Homo sapiens		
<400> 74		
atggccctcc tggccctct actggcagcc ctagtcatgc ccagctatacg ccctgtttggaa		60
tctctgggct gtatctgcc tcagaaccat ggcctactta gcaggaacac cttggtgctt		120
ctgcaccaaa tgaggagaat ctcccctttc ttgtgtctca aggacagaag agacttcagg		180

ttcccccagg	agatggtaaa	agggagccag	ttgcagaagg	cccatgtcat	gtctgtcttc	240
catgagatgc	tgcagcagat	cttcagccctc	ttccacacag	agcgctcctc	tgctgcctgg	300
aacatgaccc	tccttagacca	actccacact	ggacttcata	agcaactgca	acacctggag	360
acctgcttc	tgcaggtagt	gggagaaggag	aatctgctg	gggcatttag	cagccctgca	420
ctgaccc	ggaggtactt	ccagggaaatc	cgtgtctacc	tgaagagaa	gaaatacagc	480
gactgtgc	gggaagtgtt	cagaatggaa	atcatgaaat	ccttgttctt	atcaacaaac	540
atgcaagaaa	gactgagaag	taaagataga	gacctgggct	catcttga		588
<210>	75					
<211>	195					
<212>	PRT	/				
<213>	Homo sapiens					
<400>	75					
Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr						
1	5	10		15		
Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu						
20	25		30			
Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser						
35	40		45			
Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu						
50	55		60			
Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu						
65	70		75		80	
His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser						
85	90		95			
Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu						
100	105		110			
His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly						
115	120		125			
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg						
130	135		140			
Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser						
145	150		155		160	
Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe						
165	170		175			
Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu						
180	185		190			
Gly Ser Ser						
195						